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RAW SEQUENCE LISTING   DATE: 07/20/2001
PATENT APPLICATION: **US/09/902,460**   TIME: 11:35:19

Input Set : **N:\Crf3\RULE60\09902460.txt**
Output Set: **N:\CRF3\07202001\I902460.raw**

SEQUENCE LISTING
3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: FIDDES, J.C.
6   ABRAHAM, J.D.
8   (ii) TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH
9   FACTOR ANALOG
11   (iii) NUMBER OF SEQUENCES: 69
13   (iv) CORRESPONDENCE ADDRESS:
14   (A) ADDRESSEE: MORRISON & FOERSTER
15   (B) STREET: 755 PAGE MILL ROAD
16   (C) CITY: Palo Alto
17   (D) STATE: CA
18   (E) COUNTRY: USA
19   (F) ZIP: 94304-1018
21   (v) COMPUTER READABLE FORM:
22   (A) MEDIUM TYPE: Diskette
23   (B) COMPUTER: IBM Compatible
24   (C) OPERATING SYSTEM: Windows
25   (D) SOFTWARE: FastSEQ for Windows Version 2.0b
27   (vi) CURRENT APPLICATION DATA:
C--> 28   **(A) APPLICATION NUMBER: US/09/902,460**
C--> 29   **(B) FILING DATE: 09-Jul-2001**
30   (C) CLASSIFICATION:
32   (vii) PRIOR APPLICATION DATA:
33   (A) APPLICATION NUMBER: 09/098,628
34   (B) FILING DATE:
38 (viii) ATTORNEY/AGENT INFORMATION:
39   (A) NAME: Lehnhardt, Susan K
40   (B) REGISTRATION NUMBER: 33,943
41   (C) REFERENCE/DOCKET NUMBER: 21900-20089.10
43   (ix) TELECOMMUNICATION INFORMATION:
44   (A) TELEPHONE: 650-813-5600
45   (B) TELEFAX: 650-494-0792
46   (C) TELEX: 706141
49 (2) INFORMATION FOR SEQ ID NO: 1:
51   (i) SEQUENCE CHARACTERISTICS:
52   (A) LENGTH: 1969 base pairs
53   (B) TYPE: nucleic acid
54   (C) STRANDEDNESS: double
55   (D) TOPOLOGY: linear
57   (ii) MOLECULE TYPE: cDNA
58   (ix) FEATURE:
60   (A) NAME/KEY: Coding Sequence
61   (B) LOCATION: 970...1434
62   (D) OTHER INFORMATION:
64   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66 AATTCATGCC TCTTTCTCTC CTTTTGTTGG TAGACGACTT CAGCCTCTGT CCTTTAATTT   60

ENTERED

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67   TAAAGTTTAT GCCCCACTTG TACCCCTCGT CTTTTGGTGA TTTAGAGATT TTCAAAGCCT   120
68   GCTCTGACAC AGACTCTTCC TTGGATTGCA ACTTCTCTAC TTTGGGGTGG AAACGGCTTC   180
69   TCCGTTTTGA AACGCTAGCG GGGAAAAAAT GGGGGAGAAA GTTGAGTTTA AACTTTTAAA   240
70   AGTTGAGTCA CGGCTGGTTG CGCACGAAAA GCCCCGCAGT GTGGAGAAAG CCTAAACGTG   300
71   GTTTGGGTGG TGCGGGGGTT GGGCGGGGGT GACTTTTGGG GGATAAGGGG CGGTGGAGCC   360
72   CAGGGAATGC CAAAGCCCTG CCGCGGCCTC CGACGCGCGC CCCCCGCCCC TCGCCTCTCC   420
73   CCCGCCCCCG ACTGAGGCCG GGCTCCCCGC CGGACTGATG TCGCGCGCTT GCGTGTTGTG   480
74   GCCGAAGCCG CCGAACTCAG AGGCCGGCCC CAGAAAACCC GAGCGAGTAG GGGGCGGCGC   540
75   GCAGGAGGGA GGAGAACTGG GGGCGCGGGA GGCTGGTGGG TGTGGGGGGT GGAGATGTAG   600
76   AAGATGTGAC GCCGCGGCCC GGCGGGTGCC AGATTAGCGG ACGGCTGCCC GCGGTTGCAA   660
77   CGGGATCCCG GGCGCTGCAG CTTGGGAGGC GGCTCTCCCC AGGCGGCGTC CGCGGAGACA   720
78   CCCATCTGTG AACCCCAGGT CCCGGGCCGC CGGCTCGCCG CGCACCAGGG GCCGGCGGAC   780
79   AGAAGAGCGG CCGAGCGGCT CGAGGCTGGG GGACCGCGGG CGCGGCCGCG CGCTGCCGGG   840
80   CGGGAGGCTG GGGGGCCGGG GCCGGGGCCG TGCCCGGAGC GGGTCGGAGG CCGGGGCCGG   900
81   GGCCGGGGGA CGGCGGCTCC CCGCGCGGCT CCAGCGGCTC GGGGATCCCG GCCGGGCCCC   960
82   GCAGGGACC ATG GCA GCC GGG AGC ATC ACC ACG CTG CCC GCC TTG CCC GAG   1011
83             Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu
84              1               5                  10
86   GAT GGC GGC AGC GGC GCC TTC CCG CCC GGC CAC TTC AAG GAC CCC AAG   1059
87   Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys
88   15                20                 25                  30
90   CGG CTG TAC TGC AAA AAC GGG GGC TTC TTC CTG CGC ATC CAC CCC GAC   1107
91   Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp
92                  35                 40                  45
94   GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTA   1155
95   Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu
96                  50                 55                  60
98   CAA CTT CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT   1203
99   Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys
100                 65                 70                  75
102  GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT   1251
103  Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser
104     80                85                 90
106  AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT   1299
107  Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn
108  95                100                105                 110
110  AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA   1347
111  Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala
112                  115                120                 125
114  TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG   1395
115  Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly
116                 130                135                 140
118  CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTAAT GG   1446
119  Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
120                 145                150                 155
122  CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA   1506
123  GTAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC   1566
124  AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA   1626
125  TTCTCCCTTT TATATTGCAT CTGCTGTTAC CCAGTGAAGC TTACCTAGAG CAATGATCTT   1686
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126  TTTCACGCAT TTGCTTTATT CGAAAAGAGG CTTTTAAAAT GTGCATGTTT AGAAAACAAA   1746
127  ATTTCTTCAT GGAAATCATA TACATTAGAA AATCACAGTC AGATGTTTAA TCAATCCAAA   1806
128  AATGTCCACT ATTTCTTATG TCATTCGTTA GTCTACATGT TTCTAAACAT ATAAATGTGA   1866
129  ATTTAATCAA TTCCTTTCAT AGTTTTATAA TTCTCTGGCA GTTCCTTATG ATAGAGTTTA   1926
130  TAAAACAGTC CTGTGTAAAC TGCTGGAAGT TCTTCCGGAA TTC                     1969
132  (2) INFORMATION FOR SEQ ID NO: 2:
134      (i) SEQUENCE CHARACTERISTICS:
135          (A) LENGTH: 155 amino acids
136          (B) TYPE: amino acid
137          (C) STRANDEDNESS: single
138          (D) TOPOLOGY: linear
140     (ii) MOLECULE TYPE: protein
141      (v) FRAGMENT TYPE: internal
143     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
145  Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
146   1               5                  10                  15
147  Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
148              20                  25                  30
149  Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
150          35                  40                  45
151  Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
152      50                  55                  60
153  Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
154  65                  70                  75                  80
155  Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
156                  85                  90                  95
157  Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
158              100                 105                 110
159  Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
160          115                 120                 125
161  Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
162      130                 135                 140
163  Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
164  145                 150                 155
166  (2) INFORMATION FOR SEQ ID NO: 3:
168      (i) SEQUENCE CHARACTERISTICS:
169          (A) LENGTH: 638 base pairs
170          (B) TYPE: nucleic acid
171          (C) STRANDEDNESS: double
172          (D) TOPOLOGY: linear
174     (ii) MOLECULE TYPE: cDNA
175     (ix) FEATURE:
177          (A) NAME/KEY: Coding Sequence
178          (B) LOCATION: 91...555
179          (D) OTHER INFORMATION:
181     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
183  TGCATTTTGT GCCTTTGCTG GAAGAACCGA CTACAGGTTT GTTCAATTTC TTACAGTCTT    60
184  GAAAGCGCCA CAAGCAGCAG CTGCTGAGCC  ATG GCT GAA GGG GAA ATC ACC ACC   114
185                                   Met Ala Glu Gly Glu Ile Thr Thr
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186                                         1              5
188  TTC ACA GCC CTG ACC GAG AAG TTT AAT CTG CCT CCA GGG AAT TAC AAG   162
189  Phe Thr Ala Leu Thr Glu Lys Phe Asn Leu Pro Pro Gly Asn Tyr Lys
190      10              15              20
192  AAG CCC AAA CTC CTC TAC TGT AGC AAC GGG GGC CAC TTC CTG AGG ATC   210
193  Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile
194  25              30              35              40
196  CTT CCG GAT GGC ACA GTG GAT GGG ACA AGG GAC AGG AGC GAC CAG CAC   258
197  Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His
198              45              50              55
200  ATT CAG CTG CAG CTC AGT GCG GAA AGC GTG GGG GAG GTG TAT ATA AAG   306
201  Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys
202              60              65              70
204  AGT ACC GAG ACT GGC CAG TAC TTG GCC ATG GAC ACC GAC GGG CTT TTA   354
205  Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu
206          75              80              85
208  TAC GGC TCA CAG ACA CCA AAT GAG GAA TGT TTG TTC CTG GAA AGG CTG   402
209  Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu
210      90              95              100
212  GAG GAG AAC CAT TAC AAC ACC TAT ATA TCC AAG AAG CAT GCA GAG AAG   450
213  Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys
214  105             110             115             120
216  AAT TGG TTT GTT GGC CTC AAG AAG AAT GGG AGC TGC AAA CGC GGT CCT   498
217  Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro
218              125             130             135
220  CGG ACT CAC TAT GGC CAG AAA GCA ATC TTG TTT CTC CCC CTG CCA GTC   546
221  Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val
222              140             145             150
224  TCT TCT GAT TAAAGAGATC TGTTCTGGGT GTTGACCACT CCAGAGAAGT TTCGAGGGG   604
225  Ser Ser Asp
226              155
228  TCCTCACCTG GTTGACCCAA AAATGTTCCC TTGA                              638
230  (2) INFORMATION FOR SEQ ID NO: 4:
232      (i) SEQUENCE CHARACTERISTICS:
233          (A) LENGTH: 155 amino acids
234          (B) TYPE: amino acid
235          (C) STRANDEDNESS: single
236          (D) TOPOLOGY: linear
238     (ii) MOLECULE TYPE: protein
239      (v) FRAGMENT TYPE: internal
241     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
243  Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
244  1               5               10              15
245  Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
246              20              25              30
247  Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
248          35              40              45
249  Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
250      50              55              60
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RAW SEQUENCE LISTING   DATE: 07/20/2001
PATENT APPLICATION: **US/09/902,460**   TIME: 11:35:19

Input Set : **N:\Crf3\RULE60\09902460.txt**
Output Set: **N:\CRF3\07202001\I902460.raw**

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251   Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
252   65              70              75              80
253   Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
254              85              90              95
255   Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
256              100             105             110
257   Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
258          115             120             125
259   Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
260       130             135             140
261   Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
262   145             150             155
264   (2) INFORMATION FOR SEQ ID NO: 5:
266         (i) SEQUENCE CHARACTERISTICS:
267              (A) LENGTH: 103 base pairs
268              (B) TYPE: nucleic acid
269              (C) STRANDEDNESS: single
270              (D) TOPOLOGY: linear
273         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
275   AGAATTCAAA TATTCTGAAA TGAGCTGTTG ACAATTAATC ATCGAACTAG TTAACTAGTA    60
276   CGCAAGTTCA CGTAAAAAGG GTATCACATA TGGTACCTGC AGA                     103
278   (2) INFORMATION FOR SEQ ID NO: 6:
280         (i) SEQUENCE CHARACTERISTICS:
281              (A) LENGTH: 103 base pairs
282              (B) TYPE: nucleic acid
283              (C) STRANDEDNESS: single
284              (D) TOPOLOGY: linear
287         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
289   TCTGCAGGTA CCATATGTGA TACCCTTTTT ACGTGAACTT GCGTACTAGT TAACTAGTTC    60
290   GATGATTAAT TGTCAACAGC TCATTTCAGA ATATTTGAAT TCT                     103
292   (2) INFORMATION FOR SEQ ID NO: 7:
294         (i) SEQUENCE CHARACTERISTICS:
295              (A) LENGTH: 16 base pairs
296              (B) TYPE: nucleic acid
297              (C) STRANDEDNESS: single
298              (D) TOPOLOGY: linear
301         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
303   GAAATACACC AGTTGG                                                    16
305   (2) INFORMATION FOR SEQ ID NO: 8:
307         (i) SEQUENCE CHARACTERISTICS:
308              (A) LENGTH: 17 base pairs
309              (B) TYPE: nucleic acid
310              (C) STRANDEDNESS: single
311              (D) TOPOLOGY: linear
314         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
316   ACTTGGATCC AAAACAG                                                   17
318   (2) INFORMATION FOR SEQ ID NO: 9:
320         (i) SEQUENCE CHARACTERISTICS:
321              (A) LENGTH: 25 base pairs
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/902,460

DATE: 07/20/2001
TIME: 11:35:20

Input Set : **N:\Crf3\RULE60\09902460.txt**
Output Set: **N:\CRF3\07202001\I902460.raw**

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]